AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

Claim 1 (Withdrawn) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in a plant cell, comprising the step of introducing into said plant cell a chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in said plant cell;

b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences,

wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence that is identical to at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest,

and wherein the second of said annealing RNA sequences comprises an antisense sequence that is identical to at least 20 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest,

and wherein said DNA region comprises an intron heterologous to said sense sequence; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 2 (Withdrawn) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in a plant cell, comprising the step of introducing into said plant cell a chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in said plant cell;

b) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising

i) a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest; and

ii) an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 20 consecutive nucleotides of the sense sequence basepair with said at least 20 consecutive nucleotides of the antisense sequence,

and wherein said DNA region comprises an intron heterologous to said sense nucleotide sequence; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 3 (Withdrawn) The method of claim 2, wherein said RNA molecule further comprises a spacer nucleotide sequence located between said sense and said antisense nucleotide sequence.

Claim 4 (Withdrawn) The method of claim 2, wherein said sense nucleotide sequence comprises at least about 550 consecutive nucleotides having 100% sequence identity with at least about 550 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest.

Claim 5 (Withdrawn) The method of claim 2, wherein said nucleic acid of interest is a gene integrated in the genome of said plant cell.

Claim 6 (Previously Presented) The method of claim 5, wherein said gene is an endogenous gene.

Claim 7 (Withdrawn) The method of claim 5, wherein said gene is a foreign transgene.

Claim 8 (Withdrawn) The method of claim 2, wherein said chimeric DNA is stably integrated in the genome of said plant cell.

Claim 9 (Withdrawn) The method of claim 2, wherein said nucleic acid of interest is comprised in the genome of an infecting virus.

Claim 10 (Withdrawn) The method of claim 9, wherein said infecting virus is an RNA virus.

Claim 11 (Canceled).

Claim 12 (Withdrawn) The method of claim 2, wherein said plant cell is comprised within a plant.

Claims 13-21 (Canceled).

Claim 22 (Previously Presented) A plant cell, comprising a nucleic acid of interest, which is normally capable of being phenotypically expressed, further comprising a chimeric DNA molecule comprising the following operably linked parts:

a) a promoter, operative in said plant cell;

b) a DNA region, which when transcribed, yields an RNA molecule with at least one RNA region with a nucleotide sequence comprising

i) a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of the nucleic acid of interest; and

ii) an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of

said at least 20 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence,

and wherein said DNA region comprises an intron heterologous to said sense nucleotide sequence; and

c) a DNA region involved in transcription termination and polyadenylation.

Claims 23-25 (Canceled).

Claim 26 (Previously presented) A plant comprising the plant cell of claim 22.

Claims 27-39 (Canceled).

Claim 40 (Withdrawn) The method of claim 2, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 41 (Canceled).

Claim 42 (Previously presented) The plant cell of claim 22, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 43 (Previously Presented) The method of claim 2, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50

consecutive nucleotides having 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 44 (Previously Presented) The method of claim 2, wherein said sense nucleotide sequence includes at least 100 consecutive nucleotides having 100% sequence identity with at least 100 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 100 consecutive nucleotides having 100% sequence identity with the complement of said at least 100 consecutive nucleotides of said sense nucleotide sequence.

Claim 45 (Canceled).

Claim 46 (Previously Presented) The method of claim 43 wherein said intron is located between the DNA region encoding said sense nucleotide sequence and the DNA region encoding said antisense nucleotide sequence.

Claims 47-49 (Canceled).

Claim 50 (Withdrawn) The method of claim 44, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claims 51-52 (Canceled).

Claim 53 (Previously Presented) The plant cell of claim 22, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 54 (Previously Presented) The plant cell of claim 22, wherein said sense nucleotide sequence includes at least 100 consecutive nucleotides having 100% sequence identity with at least 100 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 100 consecutive nucleotides having 100% sequence identity with the complement of said at least 100 consecutive nucleotides of said sense nucleotide sequence.

Claim 55 (Canceled).

Claim 56 (Previously Presented) The plant cell of claim 53, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 57 (Canceled).

Claim 58 (Previously Presented) The plant cell of claim 54, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claims 59-62 (Canceled).

Claim 63 (Previously Presented) A chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a plant cell;

b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences,

wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence identical to at least 20 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest,

and wherein the second of said annealing RNA sequences comprises an antisense sequence identical to at least 20 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest,

and wherein said DNA region comprises an intron heterologous to said sense sequence; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 64 (Previously Presented) A chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a plant cell;

b) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising

i) a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest; and

ii) an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 20 consecutive nucleotides of the sense sequence basepair with said at least 20 consecutive nucleotides of the antisense sequence,

wherein said DNA region comprises an intron heterologous to said region with sense nucleotide sequence; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 65 (Previously presented) The chimeric DNA of claim 64, wherein said intron is located between part of said DNA region which when transcribed yields said sense

nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 66 (Previously Presented) The chimeric DNA of claim 64, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 67 (Previously Presented) The chimeric DNA of claim 64, wherein said sense nucleotide sequence includes at least 100 consecutive nucleotides having 100% sequence identity with at least 100 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 100 consecutive nucleotides having 100% sequence identity with the complement of said at least 100 consecutive nucleotides of said sense nucleotide sequence.

Claim 68 (Previously presented) The chimeric DNA of claim 66, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 69 (Previously presented) The chimeric DNA of claim 67, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 70 (Previously Presented) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in an isolated eukaryotic cell, comprising the step of introducing into said isolated eukaryotic cell a chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a eukaryotic cell;

b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences,

wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence identical to at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest,

and wherein the second of said annealing RNA sequences comprises an antisense sequence identical to at least 20 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest,

and wherein said DNA region comprises an intron heterologous to said sense sequence; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 71 (Previously Presented) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in an isolated eukaryotic cell, comprising the step of introducing into said isolated eukaryotic cell a chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a eukaryotic cell;

b) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising

i) a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest; and

ii) an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the

regions with sense and antisense nucleotide sequence such that said at least 20 consecutive nucleotides of the sense sequence basepair with said at least 20 consecutive nucleotides of the antisense sequence,

and wherein said DNA region comprises an intron heterologous to said region with sense nucleotide sequence; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 72 (Withdrawn) The method of claim 71, wherein said RNA molecule further comprises a spacer nucleotide sequence located between said sense and said antisense nucleotide sequence.

Claim 73 (Withdrawn) The method of claim 71, wherein said sense nucleotide sequence comprises at least about 550 consecutive nucleotides having 100% sequence identity with at least about 550 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest.

Claim 74 (Withdrawn) The method of claim 71, wherein said nucleic acid of interest is a gene integrated in the genome of said eukaryotic cell.

Claim 75 (Withdrawn) The method of claim 74, wherein said gene is an endogenous gene.

Claim 76 (Withdrawn) The method of claim 74, wherein said gene is a foreign transgene.

Claim 77 (Withdrawn) The method of claim 71, wherein said chimeric DNA is stably integrated in the genome of said eukaryotic cell.

Claim 78 (Withdrawn) The method of claim 71, wherein said nucleic acid of interest is comprised in the genome of an infecting virus.

Claim 79 (Withdrawn) The method of claim 78, wherein said infecting virus is an RNA virus.

Claim 80 (Withdrawn) The method of claim 71, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 81 (Previously Presented) The method of claim 71, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides having between 95% and 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 82 (Previously Presented) The method of claim 71, wherein said sense nucleotide sequence includes at least 100 consecutive nucleotides having 100% sequence identity with at least 100 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 100 consecutive nucleotides having 100% sequence identity with the complement of said at least 100 consecutive nucleotides of said sense nucleotide sequence.

Claim 83 (Withdrawn) The method of claim 81, wherein said intron is located between the DNA region encoding said sense nucleotide sequence and the DNA region encoding said antisense nucleotide sequence.

Claim 84 (Withdrawn) The method of claim 82, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 85 (Previously Presented) An isolated eukaryotic cell, comprising a nucleic acid of interest, which is normally capable of being phenotypically expressed, further comprising a chimeric DNA molecule comprising the following operably linked parts:

a) a promoter, operative in said eukaryotic cell;

b) a DNA region, which when transcribed, yields an RNA molecule with at least one RNA region with a nucleotide sequence comprising

i. a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of the nucleic acid of interest; and

ii. an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence,

and wherein said DNA region comprises an intron heterologous to said region with sense nucleotide sequence; and

d) a DNA region involved in transcription termination and polyadenylation.

Claim 86 (Previously presented) The eukaryotic cell of claim 85, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 87 (Previously Presented) The eukaryotic cell of claim 85, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 88 (Previously Presented) The eukaryotic cell of claim 85, wherein said sense nucleotide sequence includes at least 100 consecutive nucleotides having 100%

sequence identity with at least 100 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 100 consecutive nucleotides having 100% sequence identity with the complement of said at least 100 consecutive nucleotides of said sense nucleotide sequence.

Claim 89 (Previously Presented) The eukaryotic cell of claim 87, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 90 (Previously Presented) The eukaryotic cell of claim 88, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 91 (Previously Presented) A chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a eukaryotic cell;

b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences,

wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence identical to at least 20 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest,

and wherein the second of said annealing RNA sequences comprises an antisense sequence identical to at least 20 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest,

and wherein said DNA region comprises an intron heterologous to said sense nucleotide sequence; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 92 (Previously Presented) A chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a eukaryotic cell;

b) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising

i) a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest; and

ii) an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 20 consecutive nucleotides of the sense sequence basepair with said at least 20 consecutive nucleotides of the antisense sequence,

and wherein said DNA region comprises an intron heterologous to said region with sense nucleotide sequence; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 93 (Previously Presented) The chimeric DNA of claim 92, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 94 (Previously Presented) The chimeric DNA of claim 92, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at

least 50 consecutive nucleotides having 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 95 (Previously Presented) The chimeric DNA of claim 92, wherein said sense nucleotide sequence includes at least 100 consecutive nucleotides having 100% sequence identity with at least 100 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 100 consecutive nucleotides having 100% sequence identity with the complement of said at least 100 consecutive nucleotides of said sense nucleotide sequence.

Claim 96 (Previously Presented) The chimeric DNA of claim 94, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 97 (Previously Presented) The chimeric DNA of claim 95, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 98 (Previously Presented) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in a plant cell, comprising the step of introducing into said plant cell a chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in said plant cell;

b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences,

wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence identical to at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest,

and wherein the second of said annealing RNA sequences comprises an antisense sequence identical to at least 20 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest,

and wherein said DNA region comprises an intron ; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 99 (Previously Presented) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in a plant cell, comprising the step of introducing into said plant cell, a chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in said plant cell;

b) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising

i) a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest; and

ii) an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 20 consecutive nucleotides of the sense sequence basepair with said at least 20 consecutive nucleotides of the antisense sequence,

and wherein said DNA region comprises an intron ; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 100 (Previously Presented) A plant cell, comprising a nucleic acid of interest, which is normally capable of being phenotypically expressed, further comprising a chimeric DNA molecule comprising the following operably linked parts:

a) a promoter, operative in said plant cell;

b) a DNA region, which when transcribed, yields an RNA molecule with at least one RNA region with a nucleotide sequence comprising

i) a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of the nucleic acid of interest; and

ii) an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence,

and wherein said DNA region comprises an intron ; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 101 (Previously presented) A plant comprising the plant cell of claim 100.

Claim 102 (Previously Presented) A chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a plant cell;

b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences,

wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence identical to at least 20 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest, and wherein the second of said annealing RNA sequences comprises an antisense

sequence identical to at least 20 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest,

and wherein said DNA region comprises an intron; and

c) a DNA region involved in transcription termination and polyadenylation

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Claim 103 (Previously Presented) A chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a plant cell;

b) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising

i) a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest; and

ii) an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 20 consecutive nucleotides of the sense sequence basepair with said at least 20 consecutive nucleotides of the antisense sequence,

and wherein said DNA region comprises an intron ; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 104 (Withdrawn) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in an isolated eukaryotic cell, comprising the step of introducing into said isolated eukaryotic cell a chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a eukaryotic cell;

b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences,

wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence identical to at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest,

and wherein the second of said annealing RNA sequences comprises an antisense sequence identical to at least 20 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest,

and wherein said DNA region comprises an intron ; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 105 (Previously Presented) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in an isolated eukaryotic cell, comprising the step of introducing into said isolated eukaryotic cell a chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a eukaryotic cell;

b) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising

i) a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest; and

ii) an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 20 consecutive nucleotides of the sense sequence basepair with said at least 20 consecutive

nucleotides of the antisense sequence,

and wherein said DNA region comprises an intron ; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 106 (Previously Presented) An isolated eukaryotic cell, comprising a nucleic acid of interest, which is normally capable of being phenotypically expressed, further comprising a chimeric DNA molecule comprising the following operably linked parts:

a) a promoter, operative in said eukaryotic cell;

b) a DNA region, which when transcribed, yields an RNA molecule with at least one RNA region with a nucleotide sequence comprising

i a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of the nucleic acid of interest; and

ii an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence,

and wherein said DNA region comprises an intron ; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 107 (Previously Presented) A chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a eukaryotic cell;

b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences,

wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence identical to at least 20 consecutive

nucleotides of the nucleotide sequence of a nucleic acid of interest,

and wherein the second of said annealing RNA sequences comprises an antisense sequence identical to at least 20 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest,

and wherein said DNA region comprises an intron; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 108. (Previously Presented) A chimeric DNA comprising the following operably linked parts:

a) a promoter, operative in a eukaryotic cell;

b) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising

i) a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest; and

ii) an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 20 consecutive nucleotides of the sense sequence basepair with said at least 20 consecutive nucleotides of the antisense sequence,

and wherein said DNA region comprises an intron ; and

c) a DNA region involved in transcription termination and polyadenylation.

Claim 109 (Previously Presented) The chimeric DNA of claim 64, wherein said RNA molecule further comprises a spacer nucleotide sequence located between said sense and said antisense nucleotide sequence.

Claim 110 (Previously Presented) The chimeric DNA of claim 92, wherein said RNA molecule further comprises a spacer nucleotide sequence located between said sense and said antisense nucleotide sequences.

Claim 111 (Previously Presented) The method of claim 99, wherein said RNA molecule further comprises a spacer nucleotide sequence located between said sense and said antisense nucleotide sequences.

Claim 112 (Previously Presented) The method of claim 99, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 113 (Previously Presented) The method of claim 99, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 114 (Previously Presented) The method of claim 113, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 115 (Previously Presented) The plant cell of claim 100, wherein said RNA molecule further comprises a spacer nucleotide sequence located between said sense and said antisense nucleotide sequences.

Claim 116 (Previously Presented) The plant cell of claim 100, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide

sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 117 (Previously Presented) The plant cell of claim 100, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 118 (Previously Presented) The plant cell of claim 117, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 119 (Previously Presented) The chimeric DNA of claim 103, wherein said RNA molecule further comprises a spacer nucleotide sequence located between said sense and said antisense nucleotide sequences.

Claim 120 (Previously Presented) The chimeric DNA of claim 103, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 121 (Previously Presented) The chimeric DNA of claim 103, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 122 (Previously Presented) The chimeric DNA of claim 121, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 123 (Previously Presented) The method of claim 105, wherein said RNA molecule further comprises a spacer nucleotide sequence located between said sense and said antisense nucleotide sequences.

Claim 124 (Previously Presented) The method of claim 105, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 125 (Previously Presented) The method of claim 105, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 126 (Previously Presented) The method of claim 125, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 127 (Previously Presented) The isolated eukaryotic cell of claim 106, wherein said RNA molecule further comprises a spacer nucleotide sequence located between said sense and said antisense nucleotide sequences.

Claim 128 (Previously Presented) The isolated eukaryotic cell of claim 106, wherein said intron is located between part of said DNA region which when transcribed yields said

sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 129 (Previously Presented) The isolated eukaryotic cell of claim 106, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 130 (Previously Presented) The isolated eukaryotic cell of claim 129, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 131 (Previously Presented) The chimeric DNA of claim 108, wherein said RNA molecule further comprises a spacer nucleotide sequence located between said sense and said antisense nucleotide sequences.

Claim 132 (Previously Presented) The chimeric DNA of claim 108, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 133 (Previously Presented) The chimeric DNA of claim 108, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 134 (Previously Presented) The chimeric DNA of claim 133, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.